

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. (currently amended): A method of normalizing gene expression data ~~wherein, in a process for comparing expression quantities with respect to a plurality of genes, which expression quantities have been obtained for a first sample, and expression quantities with respect to the plurality of the genes, which expression quantities have been obtained for a second sample, with each other, data concerning the expression quantities having been obtained for the second sample are normalized,~~ the method comprising the steps of:

i) indicating ~~the~~ data concerning the expression quantities, which have been obtained for ~~the~~ a first sample and ~~the~~ a second sample, with points plotted on a logarithmic coordinate system, in which a horizontal axis represents logarithms of the expression quantities obtained for the first sample, and in which a vertical axis represents logarithms of the expression quantities obtained for the second sample,

ii) calculating a coefficient from a value of an intercept of an approximate straight line, which is obtained from approximate representation of the plotted points with a straight line having a slope of 1, on the vertical axis, and

iii) performing division processing for dividing the data concerning the expression quantities ~~with respect to the plurality of the genes, which expression quantities have been~~

~~obtained~~ for the second sample, by the coefficient, whereby the data concerning the expression quantities having been obtained for the second sample are normalized.

2. (original): A method as defined in Claim 1 wherein the first sample is a sample obtained from a normal cell, and the second sample is a sample obtained from an abnormal cell.

3. (currently amended): A method of normalizing gene expression data ~~wherein, in a process for comparing expression quantities with respect to a plurality of genes, which expression quantities have been obtained for a first sample, and expression quantities with respect to the plurality of the genes, which expression quantities have been obtained for a second sample, with each other, data concerning the expression quantities having been obtained for the second sample are normalized,~~ the method comprising the steps of:

i) indicating the data concerning the expression quantities, which have been obtained for ~~the~~ a first sample and ~~the~~ a second sample, with points plotted on a coordinate system, in which a horizontal axis represents the expression quantities obtained for the first sample, and in which a vertical axis represents the expression quantities obtained for the second sample,

ii) calculating a value of a slope of an approximate straight line, which is obtained from approximate representation of the plotted points with a straight line passing through an origin of the coordinate system, and

iii) performing division processing for dividing the data concerning the expression quantities ~~with respect to the plurality of the genes, which expression quantities have been obtained~~ for the second sample, by the value of the slope ~~of the approximate straight line,~~

whereby the data concerning the expression quantities having been obtained for the second sample are normalized.

4. (original): A method as defined in Claim 3 wherein the first sample is a sample obtained from a normal cell, and the second sample is a sample obtained from an abnormal cell.

5. (new): A method of normalizing gene expression data, the method comprising the steps of:

i) plotting a logarithmic graph of data related to a first sample versus data related to a second sample, the data related to the second sample being on a vertical axis;

ii) calculating a coefficient from an intercept formed by a straight line with a slope of 1 with a vertical axis, the straight line approximating the plotted points; and

iii) dividing the data related to the second sample by the coefficient to normalize the data for the second sample.

6. (new): A method as defined in Claim 4 wherein the first sample is a sample obtained from a normal cell, and the second sample is a sample obtained from an abnormal cell.

7. (new): A method of normalizing gene expression data, the method comprising the steps of:

i) plotting a graph of data related to a first sample versus data related to a second sample, the data related to the second sample being on a vertical axis;

ii) calculating a slope of a line through an origin, the straight line approximating the plotted points; and

iii) dividing the data related to the second sample by the slope to normalize the data for the second sample.

8. (new): A method as defined in Claim 7 wherein the first sample is a sample obtained from a normal cell, and the second sample is a sample obtained from an abnormal cell.